

Result No.	Query Match	Length	DB ID	Description
1	7	43.8	263	CCHC_BRAYA
2	7	43.8	291	YM32_MYCTU
3	7	43.8	417	PROA_MEIRU
4	7	43.8	423	CESS_HUMAN
5	7	43.8	428	Y486_MYCLE
6	7	43.8	444	VGLX_HSVB5
7	7	43.8	474	CYAL_BORPE
8	7	43.8	480	Y486_MYCTU
9	7	43.8	521	EX7L_RHILLO
10	7	43.8	603	DS26_HCWA
11	7	43.8	621	HEMI_AGAB1
12	7	43.8	742	UL47_HSVBP
13	7	43.8	777	METE_CADER
14	7	43.8	913	VGLB_PRVIF
15	7	43.8	1318	VPA14_EBV
16	7	43.8	1394	HAP_HAEIN
17	7	43.8	2390	SPCP_HUMAN
18	7	43.8	4523	DYHB_HUMAN
19	6	37.5	68	RPOZ_NEIWA
20	6	37.5	88	RPOZ_HAEIN
21	6	37.5	89	RPOZ_PASMO
22	6	37.5	90	RPOZ_VIBCH
23	6	37.5	90	RPOZ_VIBPA
24	6	37.5	90	RPOZ_VIBVO
25	6	37.5	91	RPOZ_ECOLI
26	6	37.5	91	RPOZ_XERPI
27	6	37.5	94	R28A_MYCTU
28	6	37.5	108	NIFW_RHOSH
29	6	37.5	1113	UL67_HCMVA
30	6	37.5	1117	RL18_HAEIN
31	6	37.5	1117	VGLJ_HSVSS
32	6	37.5	120	PAND_ALCEU
33	6	37.5	120	PAND_RALSTONIA

Scoring table: OLIIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41::\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1

CCMC\_BRAYA STANDARD; PRT; 263 AA.

ID CCNC\_BRAYA AC P30962;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DE Heme exporter protein C (Cytochrome c-type biogenesis protein cyc2).

GN CYC2 OR CCMC OR BLR0469.

OS Bradyrhizobium japonicum.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Bradyrhizobium; NCBI\_TAXID=375;

OX [1]

RN RP SEQUENCE FROM N.A.

RC STRAIN=J10R1F15;

RX MEDLINE-91210304; PubMed=1850420;

RA Ramsler T.M., Winteler H.V., Hennecke H.;

RT "Discovery and sequence analysis of bacterial genes involved in the biogenesis of c-type cytochromes";

RL J. Biol. Chem. 266:7793-7803(1991).

RN [2]

RN RP SEQUENCE FROM N.A.

RC STRAIN=USDA 110;

RX MEDLINE-22434998; PubMed=12597275;

RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Iriuchi M., Kawashima K., Saamoto S., Watabane A., Idesawa K., Tsuruoka H., Wada T., Yamada M., Kohara M., Matsunoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.;

RT Complete genomic sequence of Bradyrhizobium japonicum USDA110. ";

RT DNA Res. 9:189-197(2002).

RL CC -1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERiplasm FOR THE BIogenesis OF C-TYPE CYTOCHROMES.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (protable).

CC -1- SIMILARITY: BELONGS TO THE CCMC/CYC2/HELC FAMILY.

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CC DR EMBL; M60874; AAA6194.1; -

CC DR EMBL; AP05936; BAC45734.1; -

CC DR PIR; C39741; C39741.

CC DR InterPro; IPRO02541; CytC\_asm.

CC DR InterPro; IPRO3557; CytC\_biotog\_ccmc.

CC DR Pfam; PF01578; CytC\_asm; 1.

DR PRINTS; PRO1386; CCMCBIOGENESIS.

DR TIGRFPS; TIGR0191; ccmc1.

KW Cytochrome c-type biogenesis; Transport; transmembrane;

KW Inner membrane; Complete proteome.

PT	TRANSMEM	19	39	POTENTIAL.
PT	TRANSMEM	61	81	POTENTIAL.
PT	TRANSMEM	92	112	POTENTIAL.
PT	TRANSMEM	126	146	POTENTIAL.
PT	TRANSMEM	157	177	POTENTIAL.
PT	TRANSMEM	198	218	POTENTIAL.
SQ	SEQUENCE	263 AA;	28831 MW;	A02EF75765FB94EC0 CRC64;
Query Match		43.8%	Score 7;	DB 1; Length 263;
Best Local Similarity		100.0%	Pred No. 14;	
Matches		0;	Mismatches	0;
Qy		3 RAARAAA 9		
Db		151 RAARAAA 157		
<b>RESULT 2</b>				
YN32_NYCTU STANDARD; PRT; 291 AA.				
ID	YN32_NYCTU			
AC	Q10515; Q10516;			
DT	01-OCT-1996 (Rel. 34; Created)			
DT	16-OCT-2001 (Rel. 40; Last sequence update)			
DT	28-FEB-2003 (Rel. 41; Last annotation update)			
DE	HYPOTHETICAL PROTEIN			
GN	RV2232/RV2233 OR MT2292 OR MTC427.13/MTC427.14.			
OS	Mycobacterium tuberculosis			
OC	Bacteria; Actinobacteria; Actinomycetales;			
OX	Corynebacteria; Mycobacteriaceae; Mycobacterium.			
RN	NCBI_TAXID=1773;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=H37Rv;			
RX	MEDLINE=9825987; PubMed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigenthaler K., Gas S., Barry C.E. III., Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagals K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutten S., Seeger K., Skelton S., Squares S., Stables R., Sulston J.E., Taylor K., Whitehead S., Barrell G.;			
RA	Dedifferentiating the biology of mycobacterium tuberculosis from the complete genome sequence. / Nature 393:537-544(1998).			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=CDC 1551 / Oshkosh;			
RA	Pielischmann R.D., Allard D., Elsen J.A., Carpenter L., White O., Peterson J., Debay R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;			
RA	"Whole genome comparison of mycobacterium tuberculosis clinical and laboratory strains"; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation on the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
DR	EMBL; Z70632; CAA94666.1; ALT TERM.			
DR	EMBL; Z70632; CAA94655.1; ALT TERM.			
DR	TIGR; MT2293; -			
DR	Tuberulist; RV2233; -			
DR	InterPro; IPR000834; Hydrolase.			
DR	AE007074; AAC46576.1; -			
Query Match		43.8%	Score 7;	DB 1; Length 417;
Best Local Similarity		100.0%	Pred No. 21;	
Matches		0;	Mismatches	0;
Qy		6 RAARRA 12		
Db		66 RAARRA 72		
<b>RESULT 3</b>				
ID	PROA_MEIRU			
AC	Q86053;			
DT	30-MAY-2000 (Rel. 39; Created)			
DT	30-MAR-2000 (Rel. 39; Last sequence update)			
DT	28-FEB-2003 (Rel. 41; Last annotation update)			
DE	Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase) (GSA dehydrogenase).			
GN	PROA			
OS	Meiothermus ruber.			
OC	Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;			
OC	Meiothermus			
NCBI_TAXID=277;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=40;			
RA	Yaklichkin S.Y., Zimina M.S., Yurchenko Y.V., Hromov I.S., Neumikin L.V.;			
RA	"Molecular cloning and sequence analysis of the proa gene from thermophilic eubacterium thermus ruber." Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.			
RL	FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMMA-GLUTAMYL 5-PHOSPHATE INTO L-GLUTAMATE 5-SEMIALDEHYDE AND PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION TO FORM 1-PYRROLINE-5-CARBOXYLATE.			
CC	-1- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate + NADP(+) = L-gamma-glutamyl 5-phosphate + NADPH.			
CC	-1- PATHWAY: Proline biosynthesis; second step.			
CC	-1- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation on the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
DR	EMBL; AF082661; AAC72811.1; -			
DR	HRMAP; MF_00412; -; 1.			
DR	InterPro; IPR002086; Aldehyde_dehydr.			
DR	InterPro; IPR000965; Gglut_PP_reduct.			
DR	PF00111; aldedh; 1.			
DR	TIGR00407; PROA; 1.			
DR	PROSITE; PS01223; PROB; 1.			
DR	Oxidoreductase; Proline biosynthesis; NADP-oxidoreductase; Proline biosynthesis; NADP-oxidoreductase; Proline biosynthesis; NADP-oxidoreductase.			
SQ	SEQUENCE 417 AA; 44985 MW; A280A8A7E9C52268 CRC64;			
Query Match		43.8%	Score 7;	DB 1; Length 417;
Best Local Similarity		100.0%	Pred No. 21;	
Matches		0;	Mismatches	0;
Qy		4 AARRAAR 10		
Db		13 AARRAAR 19		

**RESULT 4**

CES5\_HUMAN STANDARD; PRT: 423 AA.

AC Q9BXW7; Q9NWA8; Q9NKA1;

DT 28-FEB-2003 (Rel. 4.1, Created)

DT 28-FEB-2003 (Rel. 4.1, Last sequence update)

DT 15-SEP-2003 (Rel. 4.2, Last annotation update)

DE Cat eye syndrome critical region protein 5 precursor.

GN CECRS.

OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metazoa; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TAXID=9606;

OX RN

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX MEDLINE=21275466; PubMed=11381032;

RA Footz T.K., Brinkman-Mills P., Banting G.S., Maier S.A., Riazi M.A., Bridgland L.J., Hu S., Birren B., Minoshima S., Shimizu N., Pan H., Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shauli S., Phan S., Yao Z., Chen F., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A., McDermid H.E.;

RT Analysis of the cat eye syndrome critical region in humans and the region of conserved synteny in mice: a search for candidate genes at or near the human chromosome 22 pericentromere.";

RT "NEDO human cDNA sequencing project.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Lymph;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Wagner L., Shenan C.M., Schuler G.D., Klausner R.D., Collins F.S., Farmer A.A., Rubin G.M., Bhat N.K., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek F., Brownstein M.J., Marszina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Loqueland J., Marusina K., Toshiyuki S., Carninci P., Prange C., Raha S., Worsley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Bosak S.A., Mcowan P.J., McLaren K.J., Malek J.A., Gunaratne P.H., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young P.C., Shevchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinowicz J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marrs M.A.,

RT \*Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC Event=Alternative splicing; Named isoforms=2;

CC Name=2;

CC IsoID=Q9BXW7-1; Sequence=Displayed;

CC Name=1;

CC IsoID=Q9BXW7-2; Sequence=VSP\_003840;

CC TISSUE=SPECIFICITY: Widely expressed.

CC -I- MISCCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES), a developmental disorder associated with the duplication of a 2 Mb region of 22q1.2. Duplication usually takes in the form of a supernumerary bisatellited isodicentric chromosome, resulting in

four copies of the region (represents an inv dup(22)(q11)). CES is characterized clinically by the combination of Coloboma of the iris and anal atresia with fistula, downslanting palpebral fissures, preauricular tags and/or pits, frequent occurrence of heart and renal malformations, and normal or near-normal mental development.

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CC DR EMBL; AF273271; AAK19152; 1; -;

CC DR EMBL; AF273270; AAK19151; 1; -;

CC DR EMBL; AR001034; BAA91475; 1; -;

CC DR EMBL; AR000461; BAA91280; 1; -;

CC DR EMBL; BC042540; AAH42540; 1; -;

CC DR Genew; HGNC:1843; CECR5.

CC DR InterPro; IPR006553; HAD\_CECR5.

CC DR InterPro; IPR006557; HAD\_SF\_IIA.

CC DR TIGRFAMS; TIGR04156; CECR5; 1.

CC DR TIGRFAMS; TIGR04160; HAD\_SF\_IIA; 1.

CC KW Signal, Alternative splicing.

CC FRT SIGNAL 1 23 POTENTIAL.

CC ET CHAIN 24 423 CAT EYE SYNDROME CRITICAL REGION PROTEIN

CC FRT VARSPLIC 5 MAANGCVALGAARGLCAARRAAGLQGRPARRYAVGPA

CC FRT 1 41 > MYAWPFPLPSFS (in isoform 1).

CC FRT /FTD=YSP\_003840.

CC FRT CONFLICT 54 54 D -> N (IN REF. 2; BAA91180).

CC FRT CONFLICT 86 86 V -> F (IN REF. 2; BAA91175).

CC FRT CONFLICT 297 297 E -> G (IN REF. 2; BAA91475).

CC SQ SEQUENCE 423 AA; 46321 MW; C4D9208ABBB8CCE CRC64;

Query Match Score 43.8%; Best Local Similarity 100.0%; Length 423; Matches 7;保守性 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAA 9

Db 19 RAARAA 25

RESULT 5

Y486\_MYCLC ID Y486\_MYCLC STANDARD; PRT; 428 AA.

AC P54133; Q9CB50; AC P54133; Q9CB50; Created

DT 01-OCT-1996 (Ref. 34, Last sequence update)

DT 28-FEB-2003 (Ref. 41, Last annotation update)

DE Hypothetical protein ML2443.

GN ML2443 OR U2168F OR B2168\_C2\_201.

OS Mycobacterium leprae.

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacterineae; Mycobacterium.

RN [2]

RP SEQUENCE FROM N.A.

RA Smith D.R., Robison K.; Smith D.R., Robison K.;

RL Submitted (MAR1994) to the EMBL/GenBank/DDBJ databases.

RN [1]

RP SEQUENCE FROM N.A.

RA RN [2]

RP SEQUENCE FROM N.A.

RC STRAN=TN;

RX MEDLINE=21128732; PubMed=11234002;

RA Cole S.T., Eigenthaler K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall C., Basham D., Chillingworth T., Connor R., Davies R.M., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

RA Rutter S., Seeger K., Simon S., Simmonds M., Shelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor R., Whitehead S., Woodward J.R.,  
 RA Barrell B.G., "Massive gene decay in the leprosy bacillus.";  
 RT Nature 409:1007-1011 (2001).  
 RL NATURE 409:1007-1011 (2001).  
 CC -1 SIMILARITY: TO M. TUBERCULOSIS RY0486.

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CC EMBL; U00018; AAAI228.1; ALT\_INIT.  
 DR EMBL; AL581925; CA31960.1; -.  
 DR PIR; H87214; H87214.  
 DR Leprona ML2443; -.  
 DR IPR001296; Glyco\_transf.1; 1.  
 DR Pfam; PF00534; Glycos\_lipid\_transf.1; 1.  
 DR Hypothetical protein; Complete proteome.  
 SEQUENCE 428 AA; 4521 MW; A14FF01.87E3587C CRC64;

Query Match 43.8%; Score 7; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 21; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRAARRA 8  
 Db 204 RRAARRA 210

RESULT 6  
 VOLX\_HSVBS STANDARD PRT; 444 AA.  
 ID VOLX\_HSVBS STANDARD PRT; 444 AA.  
 AC Q08103;  
 DP 01-NOV-1995 (Rel. 32, Created)  
 DP 01-NOV-1995 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glycoprotein GX precursor.  
 OS Bovine herpesvirus type 1.2 (strain ST).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=45407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 MEDLINE=94167875; PubMed=8122270;

RA Leung-Tack P., Audonnet J.F., Riviere M.;  
 RT "The complete DNA sequence and the genetic organization of the short unique region (US) of the bovine herpesvirus type 1 (ST strain)." ;  
 RT Virology 199:409-421(1994).  
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CC EMBL; 2223058; CAA80603.1; -.  
 DR PIR; S35783; S35783.  
 DR InterPro; IPR003363; Herpes\_gg.  
 DR Pfam; PF02400; Herpes\_gg; 1.  
 KW Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 444 GLYCOPROTEIN GX.  
 FT TRANSMEM 390 414 POTENTIAL.  
 FT CARBOHD 117 117 (POTENTIAL).  
 FT CARBOHD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SEQUENCE 444 AA; 46708 MW; 0145942AA35B05CB CRC64;

Query Match 43.8%; Score 7; DB 1; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AARRA 14  
 Db 422 AARRA 428

RESULT 7  
 CYAE\_BORPE STANDARD PRT; 474 AA.  
 ID CYAE\_BORPE  
 AC P11092;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein cyae Precursor.  
 GN CYAE.  
 OS Bordetella pertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetellales.  
 OX NCBI\_TaxID=520;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=1823;  
 RX MEDLINE=9909151; PubMed=2905265;

RA Sakamoto H., Bellalou J., Ullmann A., Danchin A.;  
 RT "Secretion of cyclolin, the calmodulin-sensitive adenylate cyclase-haemolysin bifunctional protein of Bordetella pertussis." ;  
 RL EMBO J. 7:3997-4004(1988).  
 CC -1 FUNCTION: CYAE IS NECESSARY FOR TRANSPORT OF CALMODULIN-SENSITIVE ADENYLATE CYCLASE-HEMOLYSIN (CYCLOLYSIN).  
 CC -1 SUBCELLULAR LOCATION: Outer membrane (By similarity).  
 CC -1 SIMILARITY: BELONGS TO THE PRPF FAMILY OF SECRETION PROTEINS.

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CC DR EMBL; X14199; CAA32414.1; -.  
 DR PIR; S02388; BYBRCE.  
 DR InterPro; IPR003423; OEP.  
 DR Pfam; PF02321; OEP; 2.  
 KW Hemolysis; Transport; Outer membrane; Signal.  
 FT SIGNAL 1 31 POTENTIAL.  
 FT CHAIN 32 474 PROTEIN CYAE.  
 SQ SEQUENCE 474 AA; 50204 MW; 29A4F21D77FC957 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 23; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AARRA 14  
 Db 203 AARRA 209

RESULT 8  
 Y486\_MYCTU STANDARD PRT; 480 AA.  
 ID Y486\_MYCTU  
 AC Q11152;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein Rv0466.  
 GN Rv0466 OR MT0504 OR MTIC2UG9-12.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinomycetales;

*Corynebacterineae*; *Mycobacteriaceae*; *Mycobacterium*.  
NCBI TaxID:1773;

RC	STRAIN=MAFF303099;	PUBMED=11214968;
RX	MEDLINE=2108930;	PubMed=11214968;
RA	Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,	
RA	Watanebe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,	
RA	Kishida Y., Miyakawa C., Kohara M., Matsumoto M., Matsuno A.,	
RA	Mochizuki Y., Nakayama S., Yamada M., Tabata S., Sugimoto M.,	
RA	Takeuchi C., Yamada N., Nakazawa N., Shimo S., Sugimoto M.,	
RA	"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";	
RT	DNA Res. 7:331-338(2000).	
RT	-1 - FUNCTION: Bidirectionally degrades single-stranded DNA into large	
CC	acid-insoluble oligonucleotides, which are then degraded further	
CC	into small acid-soluble oligonucleotides (By similarity).	
CC	-1 - CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5' - to 3' -	
CC	or 3' - to 5' - direction to yield nucleoside 5'-phosphates.	
CC	-1 - SUBUNIT: Heterooligomer composed of large and small subunits (By	
CC	similarity).	
CC	-1 - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	
CC	-1 - SIMILARITY: BELONGS TO THE XSP family.	
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CC	EMBL: AP003010; BAB53037.1; - .	
DR	HAMAP; MF_00378; ; 1.	
DR	InterPro; IP0003753; Exonuc_VII_L.	
DR	InterPro; IP0004365; tRNA_Anti.	
DR	PFAM; PF02601; Exonuc_VII_L; 1.	
DR	Pfam; PF01336; tRNA_Anti; 1.	
DR	TIGRFAMS; TIGR00237; xseA; 1.	
KW	Hydrolease; Nuclease; Exonuclease; Complete proteome.	
SO	SEQUENCE 521 AA; 5617 MW; 6DDE75D12DF085 CRC64;	
Query Match	43.8%; Score 7; DB 1; Length 521;	
Best Local Similarity	100.0%; Pred. No. 25;	
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 AARRAAR 10	
DB	305 AARRAAR 312	
RESULT 10		
US926_HCMVA		
ID US26_HCMVA		
STANDARD;		
PRP;	603 AA.	
AC P09699		
DT 01-MAR-1989 (Rel. 10, Created)		
DT 01-FEB-1991 (Rel. 10, Last sequence update)		
DT 01-FEB-1991 (Rel. 17, Last annotation update)		
DE Hypothetical protein HMLF5.		
GN US26.		
OS Human cytomegalovirus (strain AD169);		
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
NCBI TAXID=0360;		
OX [1]		
RN		
RP	SEQUENCE=87169717; PubMed=3031311;	
RA	Weston R., Barrell B.G.;	
RA	Sequence of the short unique region, short repeats, and part of the	
RT	long repeats of human cytomegalovirus.;	
RL J. Mol. Biol. 192:177-208(1986).		
RN	COMPLETE GENOME.	
RA	MEDLINE=90269039; PubMed=2161319;	
RA	Che M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,	
[2]	Hutchison C.A. III, Kouzrides T., Martignetti J.A.,	
RA	Horrell T., Hutchison C.A. III, Kouzrides T., Martignetti J.A.,	
RA	Preddie E., Hatchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.,	
RA	SEQUENCE FROM N.A.	
[1]	Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
[1]	SEQUENCE FROM N.A.	
[1]	NCBI_TAXID=1773;	
SEQUENCE FROM N.A.		
STRAIN=H37RV;		
MEDLINE=9825987;	PUBMED=9634230;	
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,		
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Hickey E.,		
Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,		
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,		
Oliver S., Osborne J., Quail M.A., Rajandren M.A., Rogers J.,		
Rutter S., Seeger K., skeleton S., Squares S., Squares R.,		
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,		
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";		
Nature 393:537-544(1998).		
[2]	SEQUENCE FROM N.A.	
STRAIN=CDC 1551 / Oshkosh;		
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,		
Peterson J., DeBoy R., Dodson R., Grind L.I., Haft D., Hickey E.,		
Kolonay J.F., Benson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,		
DeJong A., Utterback T., Weidman J., Khouli H., Gill J., Mikula A.,		
Bishai W.,		
"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";		
Submitted (APR-2001) to the EMBL/GenBank/DDJBJ databases.		
[1]	SIMILARITY: TO MLEPRAE ML2443.	
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EMBL: 277162; CAB00947.1; - .		
EMBL: AE005951; AAK44727.1; - .		
PIR: A70744; A70744.		
TIGR: MT0504; - .		
Tubercolist; Rv0486; - .		
InterPro; IPR001296; Glyco_trans_1.		
pfam; PF00334; Glycos_transf_1.		
HYPOTHETICAL PROTEIN; Complete Proteome.		
SEQUENCE 480 AA; 50541 MW; 2134755E894A9CCF CRC64;		
Query Match	43.8%; Score 7; DB 1; Length 480;	
Best Local Similarity	100.0%; Pred. No. 23;	
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
2 RRAARRAA 8		
1        252 RRAARRAA 258		
RESULT 9		
EX7L_RHIL0	STANDARD;	PRT;
Q98743;		521 AA.
28-FEB-2003 (Rel. 41, Created)		
28-FEB-2003 (Rel. 41, Last sequence update)		
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6) (Exonuclease VII large subunit).		
XSE OR MU16896.		
Rhizobium loti (Mesorhizobium loti).		
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Mesorhizobium.		
[1]	SEQUENCE FROM N.A.	



METE\_CAUCA  
ID METE\_CAUCA STANDARD; PRT; 777 AA.  
AC O9AAW1;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase  
DE (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)  
DE (Cobalamin-independent methionine synthase).  
GN METE OR CC0482.  
OS Caulobacter crescentus; Bacteria; Proteobacteria; Caulobacterales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_Taxid=155892;  
RN [1] PRODENCE FROM N.A.  
RP STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson W.C., Newton A., Stephanus C., Phadke N.D., Ely B.,  
RA Daboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khourel H., Sherry J., Berry K.,  
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).  
CC -I- FUNCTION: Catalyzes the transfer of a methyl group from 5'-  
methyldihydrofolate to homocysteine resulting in methionine  
formation (BY similarity).  
CC -I- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyl-L-glutamate + L-  
homocysteine = tetrahydropteroyl-L-glutamate + L-methionine.  
CC -I- COFACTOR: Zinc; binds one ion per subunit (BY similarity).  
CC -I- PATHWAY: Terminal step in the de novo biosynthesis of methionine.  
CC -I- SIMILARITY: Belongs to the 'vitamin-B12 independent methionine  
synthase' family.

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CC EMBL: AE005721; AAC22469.1; -;  
DR PIR: A87309; A87309.  
DR TIGR; CC0482; -;  
DR HAMAP; MF\_00172; -; 1.  
DR InterPro; IPR002629; Methionine\_synt. 1.  
DR InterPro; IPR006276; Met\_Syn\_B12.ind.  
DR Pfam; PF004692; Methionine\_synt. 2.  
DR TIGRFAMS; TIGR01371; met\_synth\_B12.ind.  
KW Transferase; Methyltransferase; Methionine biosynthesis; zinc; Repeat; Complete proteome.  
FT METAL 665. ZINC (BY SIMILARITY).  
FT METAL 667. ZINC (BY SIMILARITY).  
FT METAL 750. ZINC (BY SIMILARITY).  
SQ SEQUENCE 777 AA; 84380 MW; 1C4DSFD/B80A80F3 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 777;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AARRA 14  
Db 770 AARRA 776

AC P08355; (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-AUG-1988 (Rel. 08, Last annotation update)  
DE Glycoprotein GII precursor.  
OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_Taxid=31523;  
RN [1] RP SEQUENCE FROM N.A.  
RX MEDLINE=87284143; PubMed=3039163;  
RA Robbins A.K., Dorney D.J., Wathen M.W., Whealy M.E., Gold C.,  
RA Watson R.W., Holland L.E., Weed S.D., Levine M., Glorioso J.C.,  
RA Enquist L.W.;  
RT "The Pseudorabies virus GII gene is closely related to the gB glycoprotein gene of herpes simplex virus." related to the gB glycoprotein gene of herpes simplex virus.  
RL J. Virol. 61:2691-2701(1987).  
RN [2] RP SEQUENCE OF 847-913 FROM N.A.  
RX MEDLINE=89219298; PubMed=25437777;  
RA Simon A., Netterleiter T.C., Rzila H.J.;  
RA "Pseudorabies virus displays variable numbers of a repeat unit adjacent to the 3' end of the glycoprotein GII gene.";  
RL J. Gen. Virol. 70:1239-1246(1989).  
RN [3] RP EXPORT PATHWAY; PubMed=2157862;  
RX MEDLINE=90219190; PubMed=2157862;  
RA Whealy M.E., Robbins A.K., Enquist L.W.;  
RT "The export pathway of the pseudorabies virus gB homolog GII involves oligomer formation in the endoplasmic reticulum and protease processing in the Golgi apparatus."  
RL J. Virol. 66:1946-1955(1992).  
CC -I- SUBUNIT: DIMER; PROBABLY LINKED BY DISULFIDE BONDS.  
CC -I- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.  
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CC EMBL: M17321; AAC7465.1;  
DR EMBL; D00464; BA00359.1; -;  
DR PIR: A291159; VGBEPS;  
DR InterPro; IPR00234; Glycoprot\_B.  
DR Pfam; PF00606; Glycoprotein\_B; 1.  
DR PRODom; PD000693; Glycoprot\_B; 1.  
DR Glycoprotein; Transmembrane; Signal.  
KW FT SIGNAL 1 40  
FT CHAIN 41 913  
FT DOMAIN 41 750  
FT TRANSMEM 751 819  
FT DOMAIN 820 913  
FT CARBOHYD 151 151  
FT CARBOHYD 151 151  
FT CARBOHYD 261 261  
FT CARBOHYD 441 441  
FT DOMAIN 516 516  
FT CARBOHYD 573 573  
FT CARBOHYD 633 633  
FT CARBOHYD 697 697  
SQ SEQUENCE 913 AA; 100234 MW; 5D60D35E855437 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 913;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AAARRR 13  
Db 495 AAARRR 501

RESULT 15

VP14\_EBV STANDARD; PRT; 1318 AA.

ID VP14\_EBV  
 AC P03175;  
 DR 21-JUN-1986 (Rel. 01, Created)  
 DR 21-JUN-1986 (Rel. 01, Last sequence update)  
 DR 01-APR-1993 (Rel. 25, Last annotation update)  
 DS probable membrane antigen P140 ( tegument protein).

GN BNRFL1

OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).

OC viruses; dsDNA viruses, no RNA stage; Herpesviridae;

CC Gammaherpesvirinae; Lymphocryptovirus.

OX NCBI\_TAXID:10377;

RN [1]

RP COMPLETE GENOME.

RX MEDLINE:8427666; PubMed:6087149;

RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnall P.S., Barrell B.G.;

RA RT DNA sequence and expression of the B95-8 Epstein-Barr virus genome.;

RN Nature 310:207-211(1984).

RN [2]

RP SEQUENCE FROM N. A.

RX MEDLINE:8604599; PubMed:2998073;

RA Hudson G.S., Bankier A.T., Satchwell S.C., Barrell B.G.;

RA RT The short unique region of the B95-8 Epstein-Barr virus genome.;

RL Virology 147:81-98(1985).

CC -!- FUNCTION: tegument protein.

CC -!- SIMILARITY: TO BOTH 140 kDa MEMBRANE ANTIGEN ENCODED AT THE EXTREMITIES OF THE HERPESVIRUS SAIMRI GENOME (3 AND 75/EIPL1).

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CC EMBL; V01555; CAA24862.1;  
 DR EMBL; M11924; AAA45899.1;  
 DR PIR; A03740; Q00741;  
 DR InterPro; IPR000728; AIRS-related.  
 DR Pfam; PF02769; AIRS\_C\_1.  
 RW Membrane; Antigen; Late Protein; Structural protein.

SEQUENCE 1318 AA; 142843 MW; 58D1DC644EBE6\_CRC64;  
 SQ

Query Match	43.8%	Score	7	DB	1	Length	1318
Best Local Similarity	100.0%	Pred.	No.	53			
Matches	7	Conservative	O:	Mismatches	0;	Gaps	0;
Indels							

OY 5 ARAAARR 11  
 DB 322 ARAAARR 328

Search completed: August 9, 2003, 16:29:52  
 Job time : 9.22857 secs